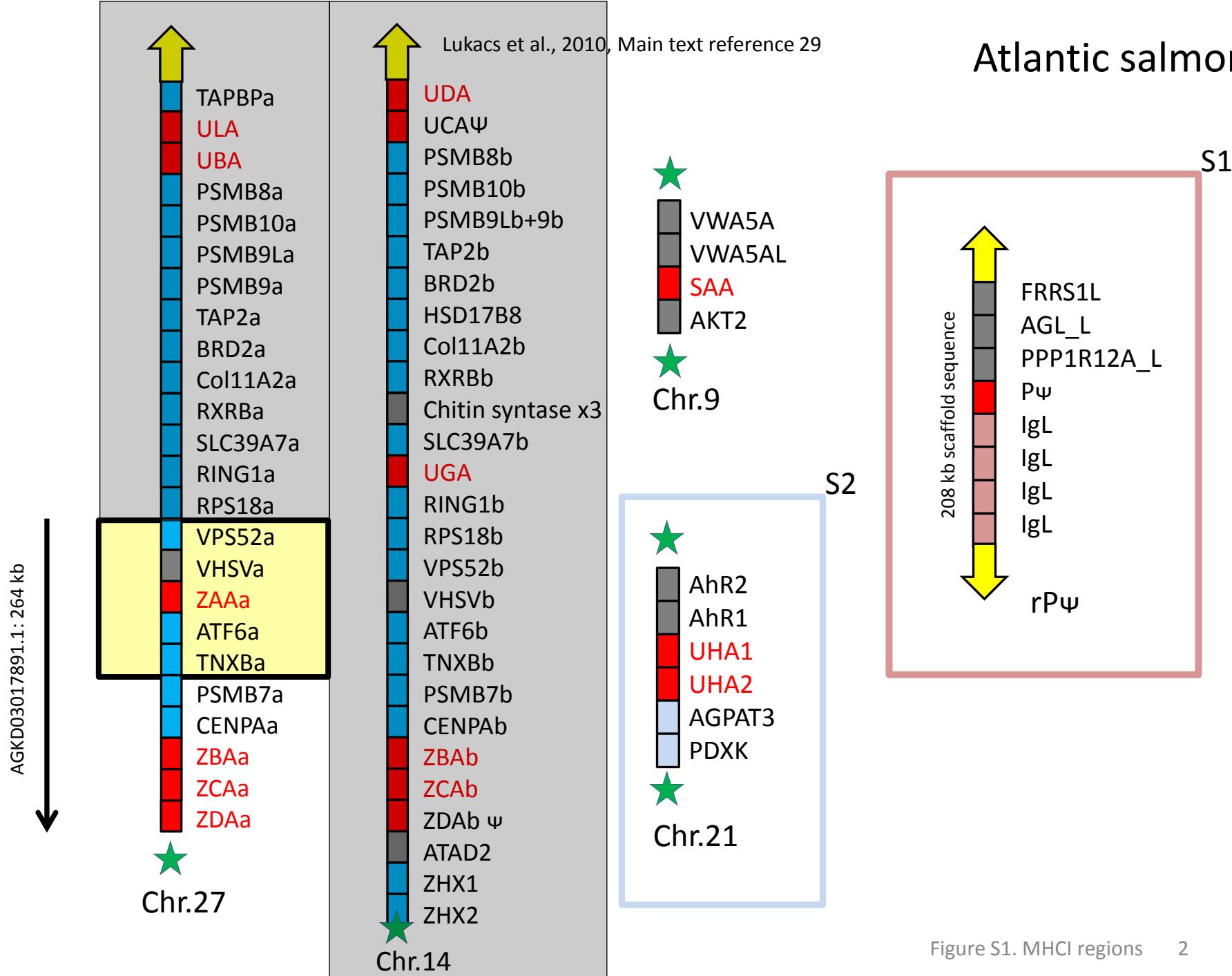


# Additional file 1: Figure S1. Ray-finned fish MHC class I regions

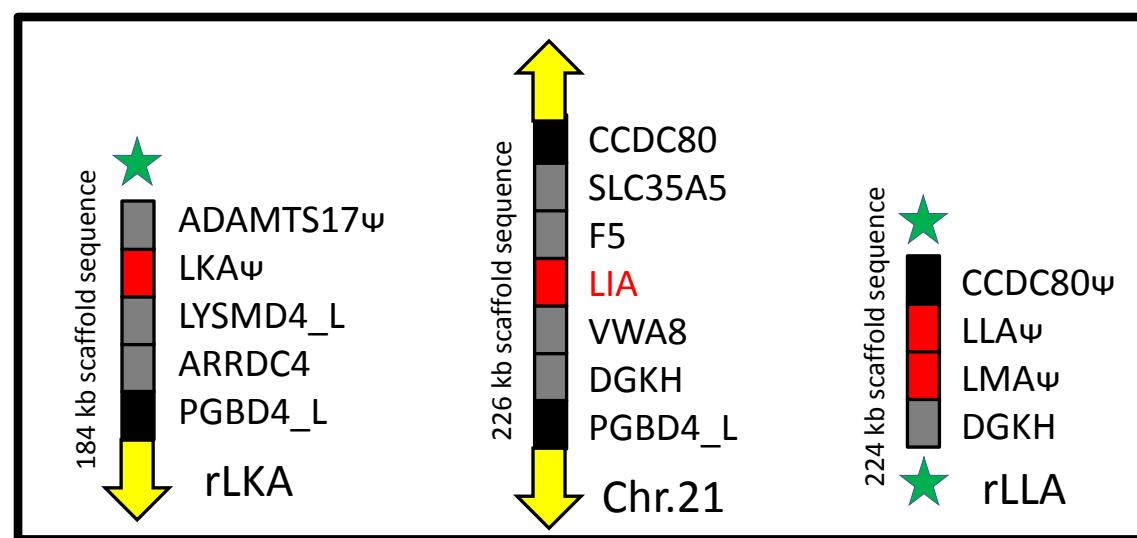
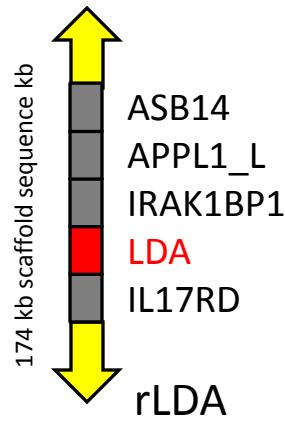
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Cavefish ( <i>Astyanx mexicanus</i> ) MHC class I regions	4
Zebrafish ( <i>Danio rerio</i> ) MHC class I regions	5
Medaka ( <i>Oryzias latipes</i> ) MHC class I regions	6
Platyfish ( <i>Xiphophorus maculatus</i> ) MHC class I regions	7
Tilapia ( <i>Oreochromis niloticus</i> ) MHC class I regions	8
Stickleback ( <i>Gasterosteus aculeatus</i> ) MHC class I regions	9
Tetraodon ( <i>Tetraodon nigroviridis</i> ) MHC class I regions	10
Fugu ( <i>Takifugu rubripes</i> ) MHC class I regions	11
Spotted gar ( <i>Lepisosteus oculatus</i> ) MHC class I regions	12

**Figure legend:** The genomic surroundings of MHC class I genes in ten fishes are shown with genes represented by blocks. Data were derived from the Ensembl database, except those of Atlantic salmon (Additional file 3: Text S1). Several genes flanking the MHC class I genes were identified using the Ensembl genome browser and, in some cases, gene prediction software. Identities of all genes without Ensembl annotation were investigated by blasting their deduced products against GenBank. When identity was uncertain, phylogenetic analysis (Neighbor Joining method) was performed. Sequences with somewhat questionable sequence identity and members of complex gene families were given the name extension “–like” (\_L), while those without good match were defined as not determined (n.d.) and mostly omitted for space purposes. Names of genomic regions and MHCI genes used in this study are often simplified references to species and Ensembl scaffolds/contigs or linkage groups/chromosomes, with details given vertically. For precise location of individual MHC genes see Additional files 2:Table S1, 3:Text S1 and 4:Text S2. Yellow arrows indicate availability of information on extensions of the depicted region fragments, while green stars indicate absence of such information. Black line linking rectangles represent regional gaps where the distance is shown. Red line linking rectangles represent a continuous region introduced due to space problems. Please be aware that some gene families such as the zinc finger protein family (ZNF) can be extensively dispersed throughout the genome and that their shared presence is not a good indication for regional synteny. Further colorings of individual genes are as follows: orange= MHC class II, red= MHC class I, blue= MHC region scaffold genes as found in human, gray= other Genes and black=genes found in the fugu5 assembly. Presumable pseudogenes are marked with ψ, and names of MHCI genes with evidence of transcription (Table S1, Text S1) are in red font. Zebrafish D8.46A refers to an MHC class II gene described in Dijkstra et al. [main text reference 19]. The black arrow pointing at region rTR4 indicates position of P-gene in syntenic tetraodon rTN3 scaffold. Regions published previously are shown with grey boxes and reference. The Atlantic salmon region boxed and shaded yellow represents an overlap between the previously published BAC sequence (Lukacs et al.[main text reference 29]) and the genome scaffold sequence. Lineages or alternative gene names are shown in parenthesis. When information on chromosomal location is missing, the region has been provided with an R prior to the first MHCI gene of that region. Regions with syntenic genes are boxed with identical colors, syntenic genes as rectangles in same color and marked S1 through S11. Regions with one MHCI gene only are not shown.

# Atlantic salmon

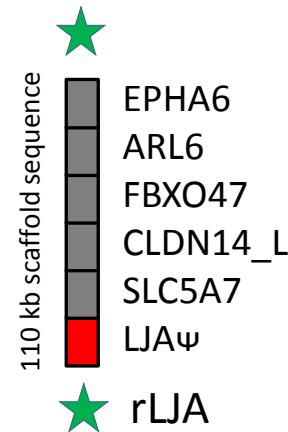
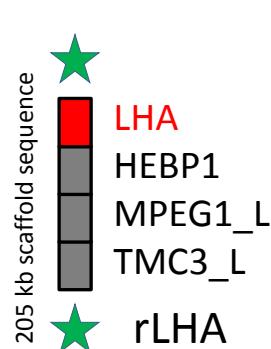
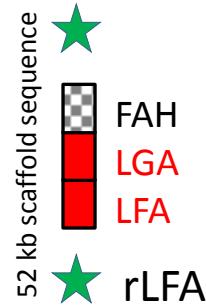
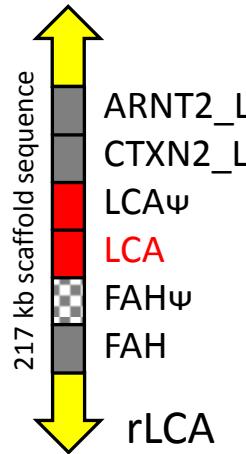


# Atlantic salmon cont.



(Lien et al.2011  
Main text reference 68)

S4



# Cavefish

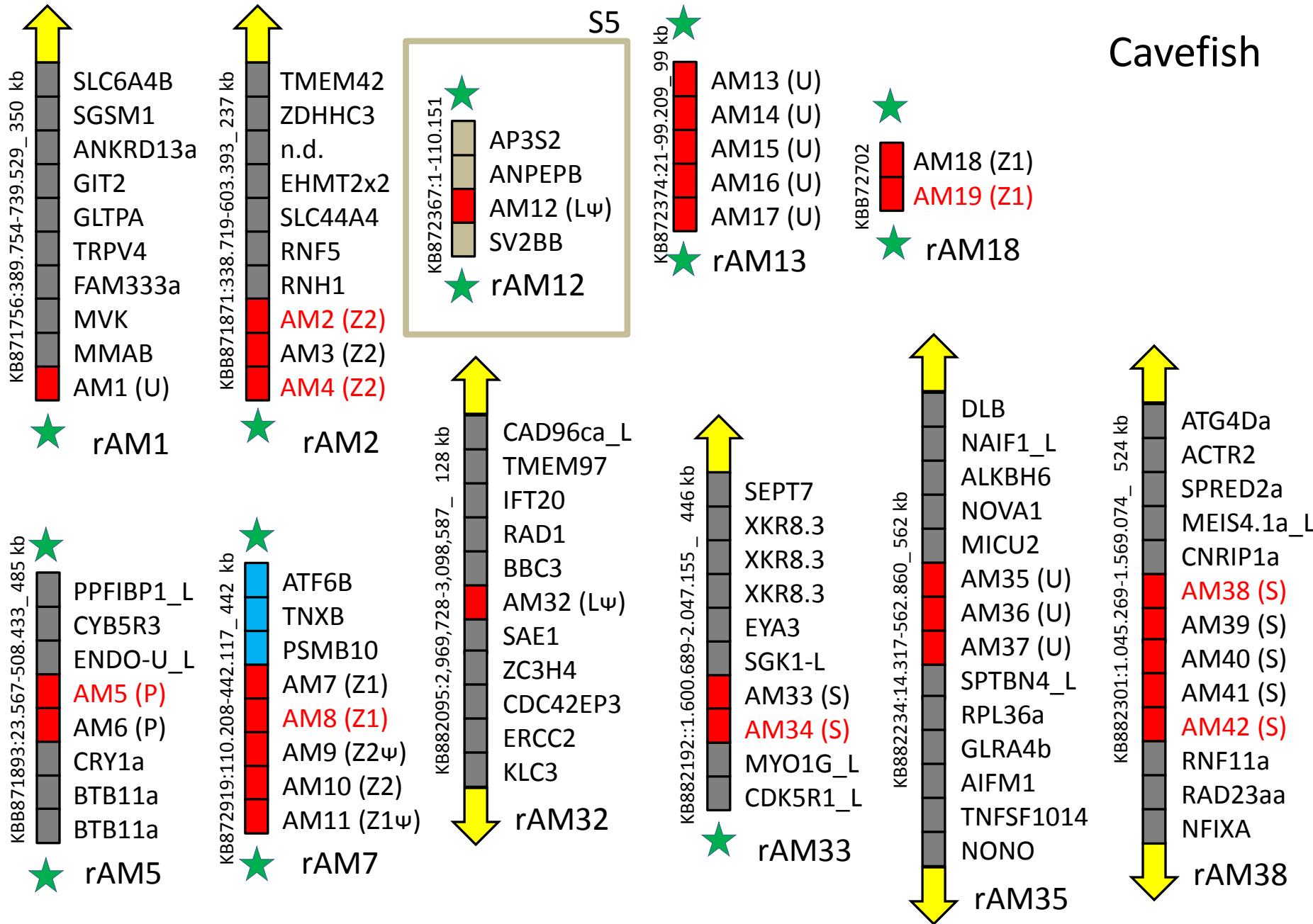


Figure S1. MHC I regions

# Zebrafish

S5

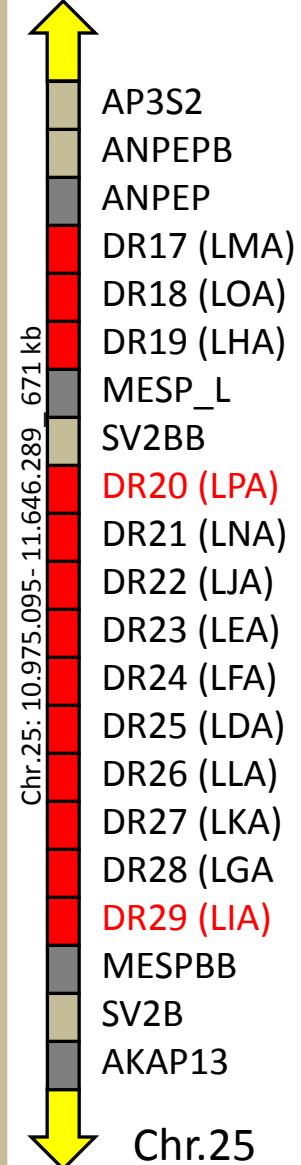
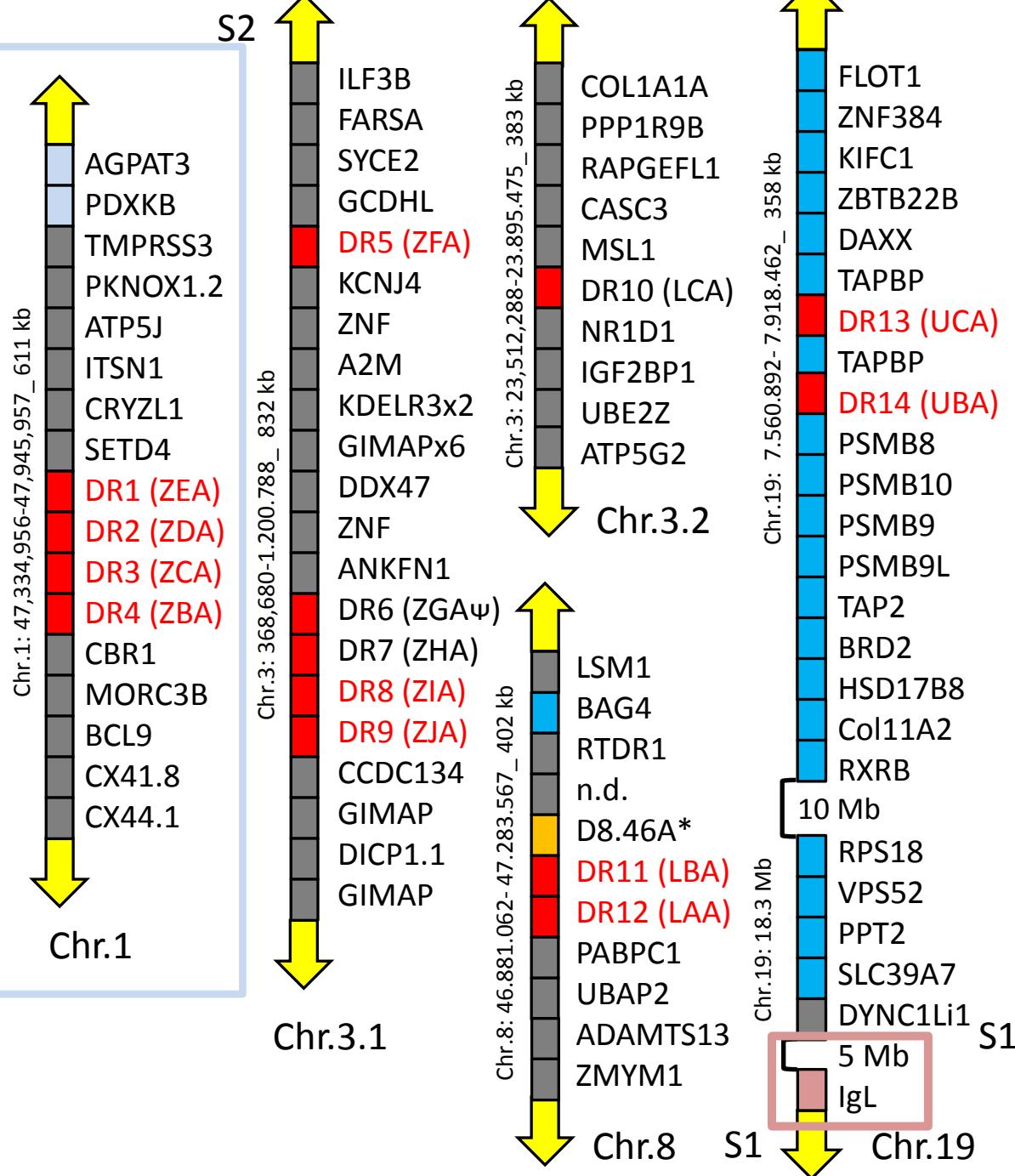
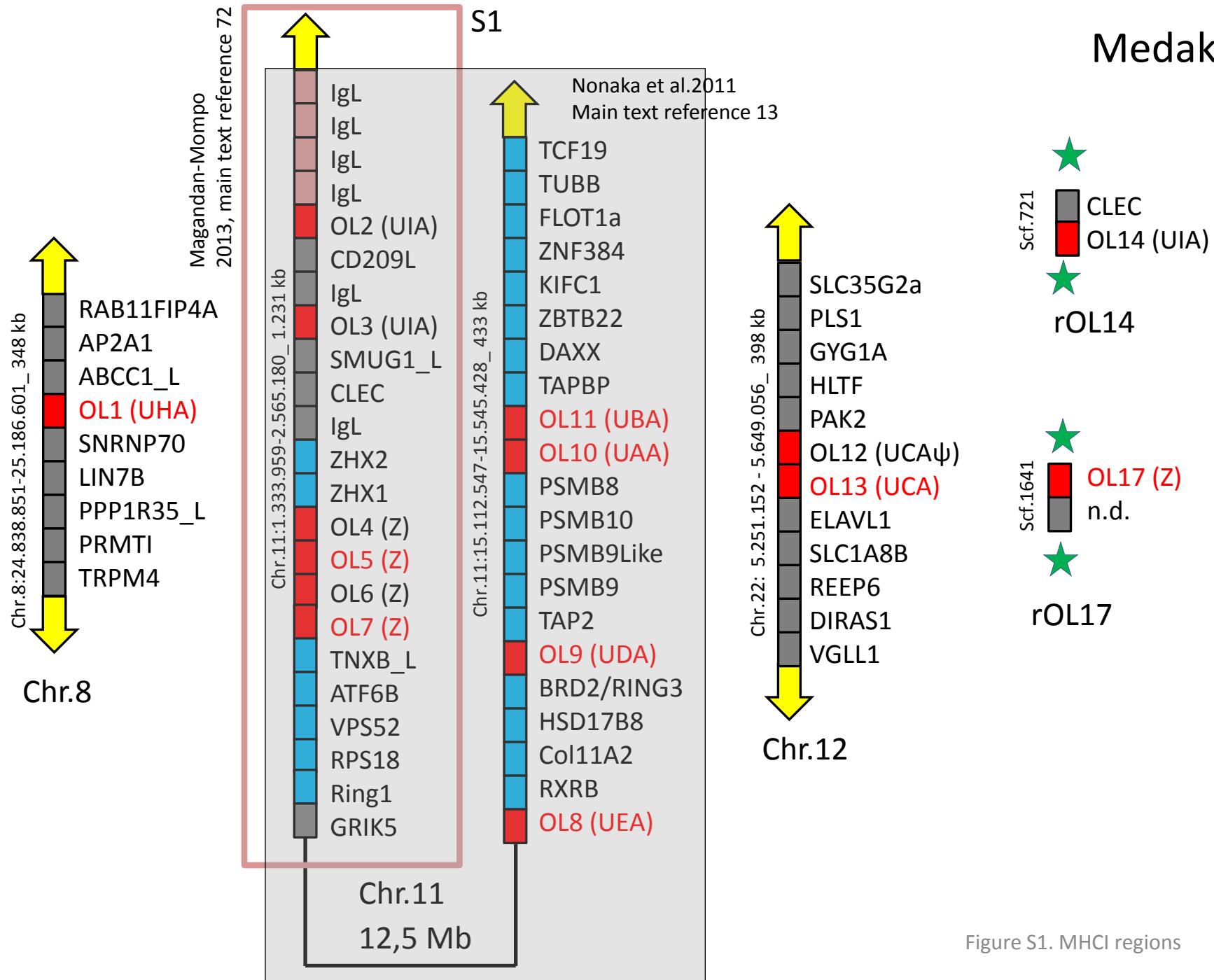


Figure S1. MHCI regions

5



# Medaka



# Platyfish

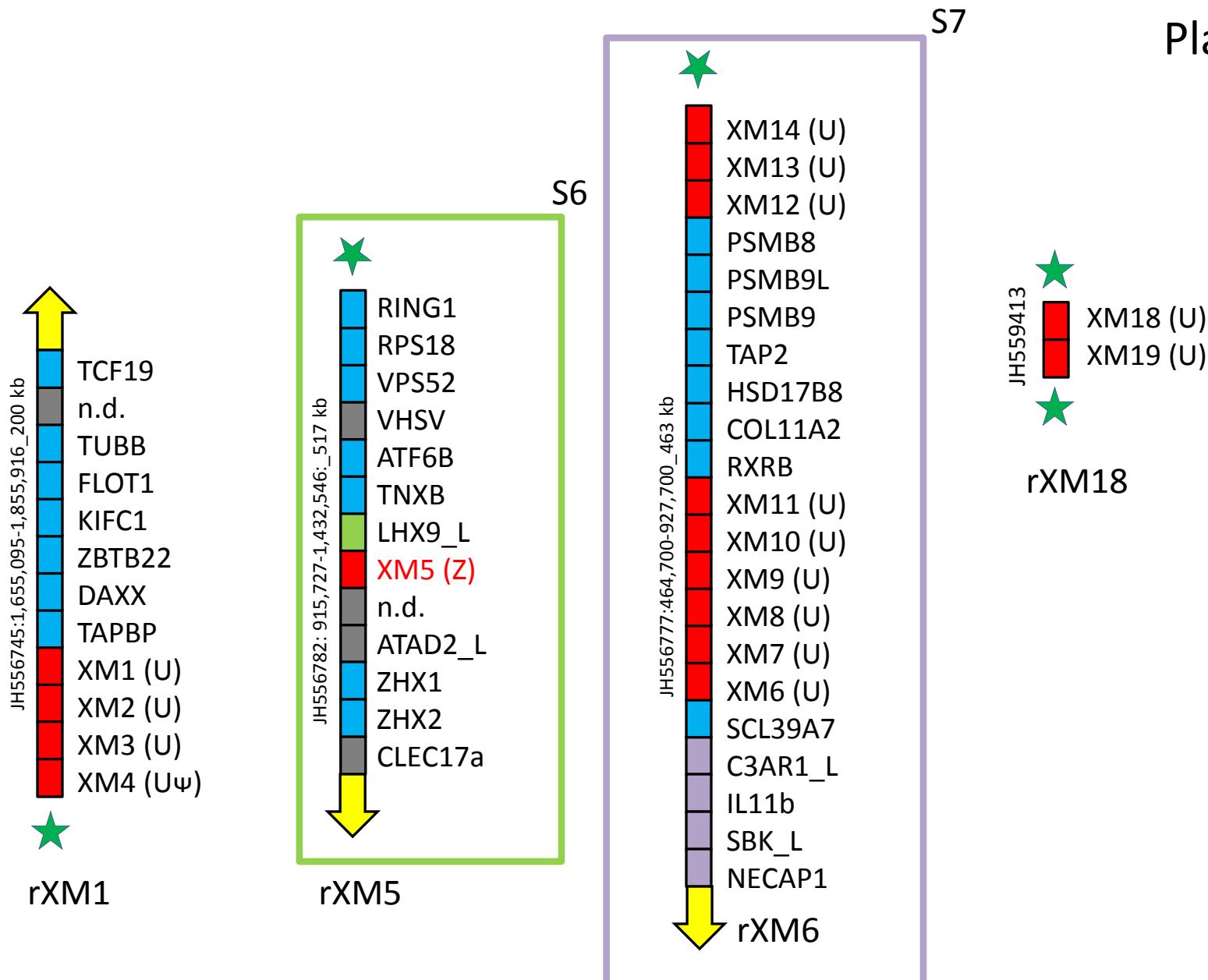
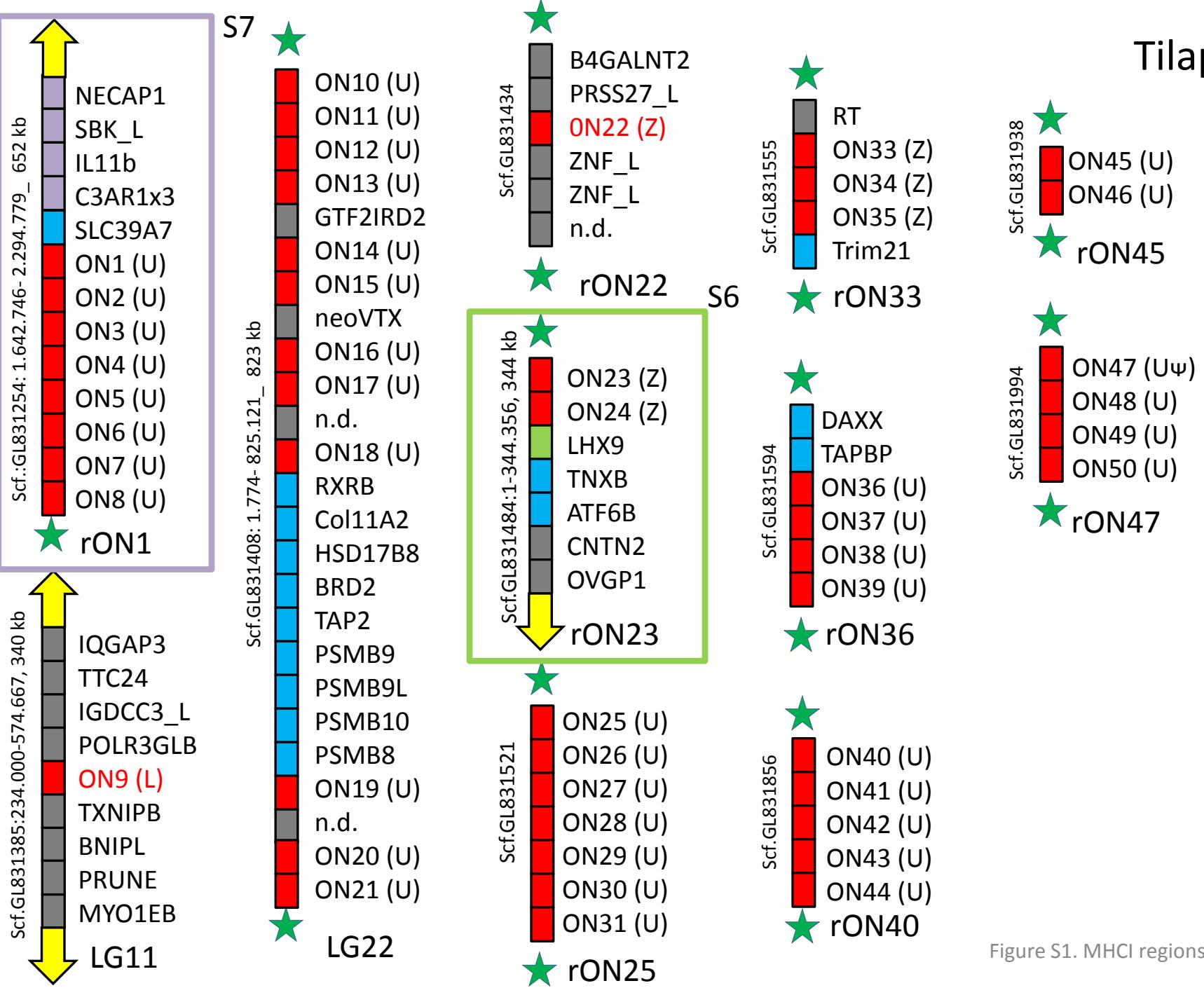
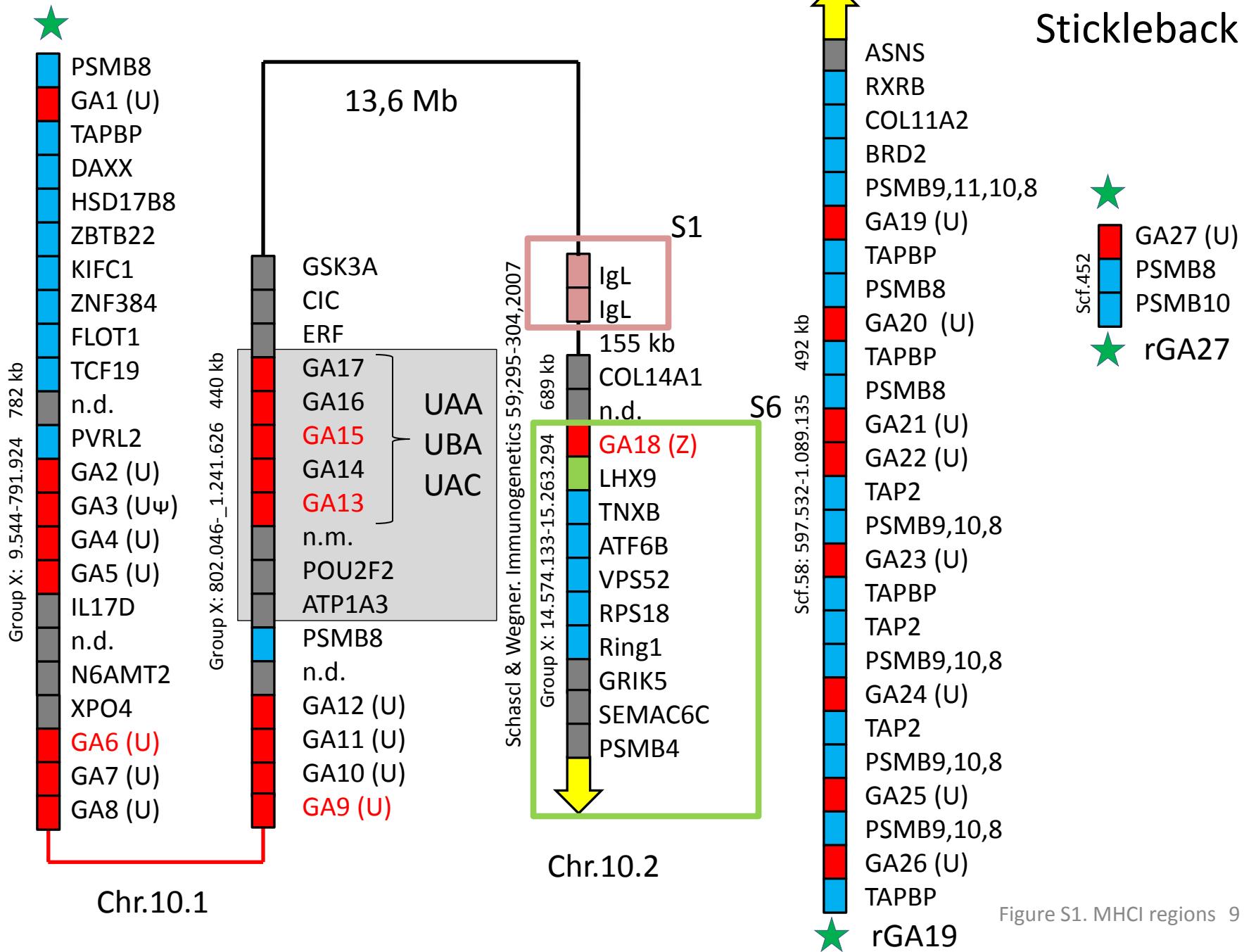


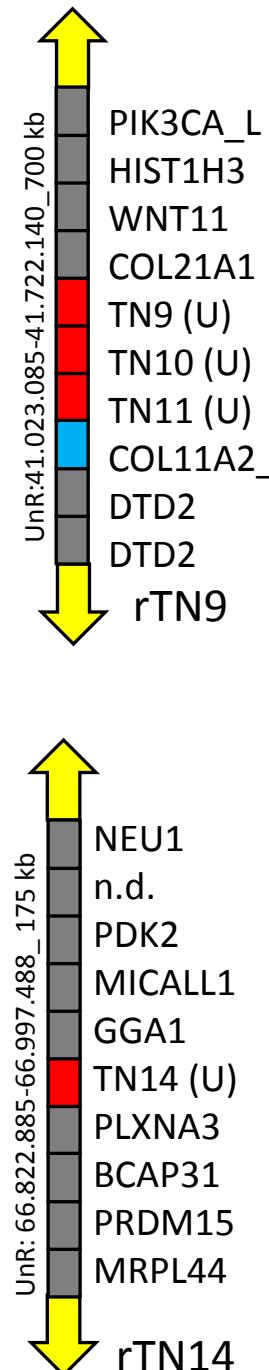
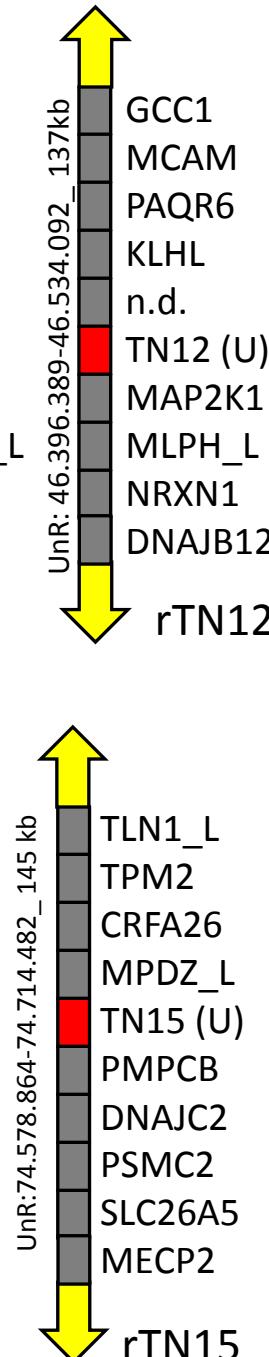
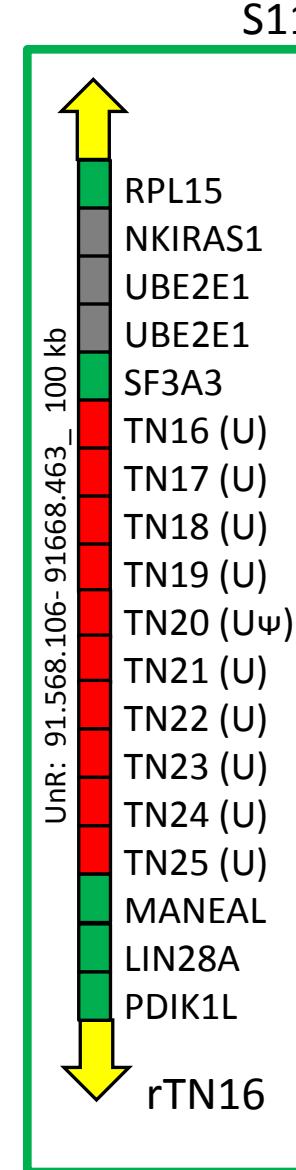
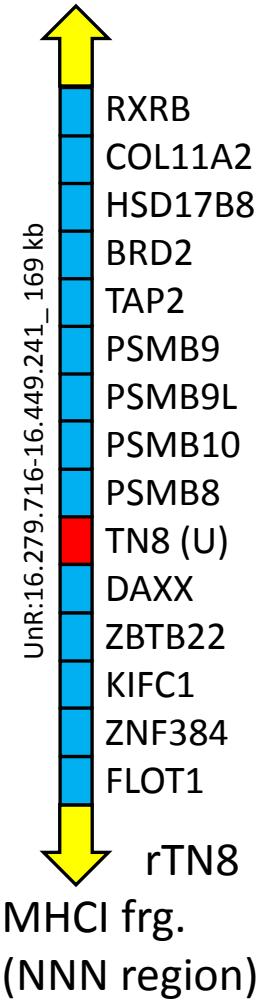
Figure S1. MHC regions

# Tilapia





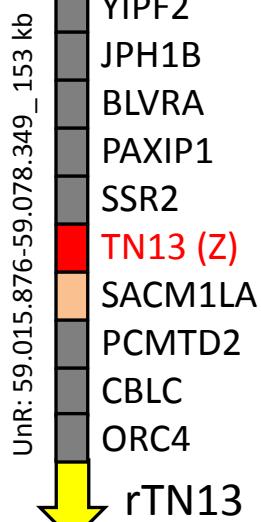
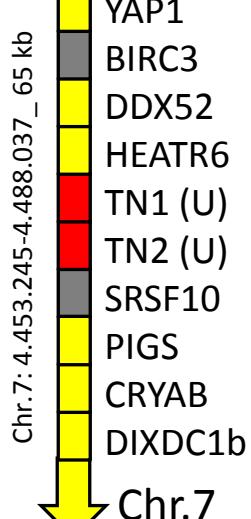
# Tetraodon



S10

S8

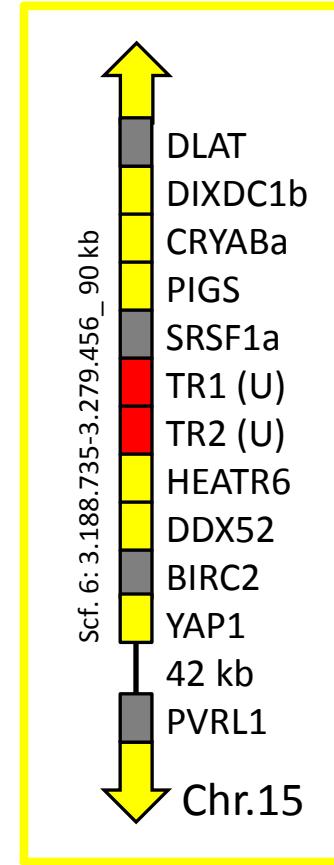
S9



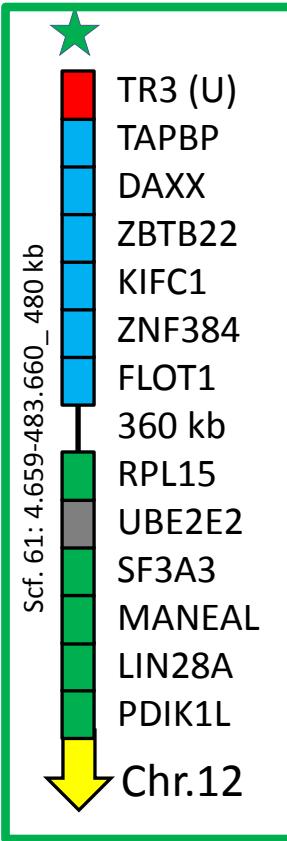
Clark et al.2001, main text reference 53; BAC GSS sequences

	★
U	U C C U
U	PSMB8
U	PSMB10
U	PSMB10
U	PSMB9L
U	PSMB9
TAP2	
HSD17B8	
BRD2	
Col11A2	
Col11A2	
U	
RXRB	
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U	
U	
PSMB8	
U	
U	
TAPBP	
ZNF297	
KNSL2	
FLOT1	

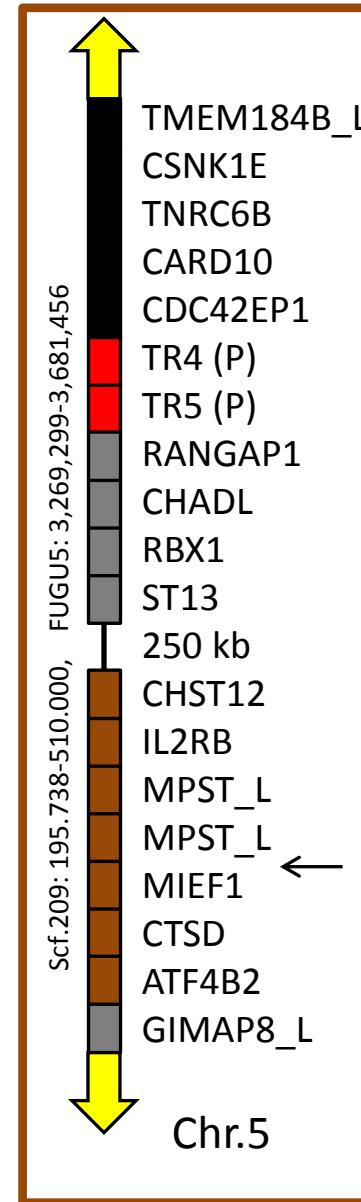
S8



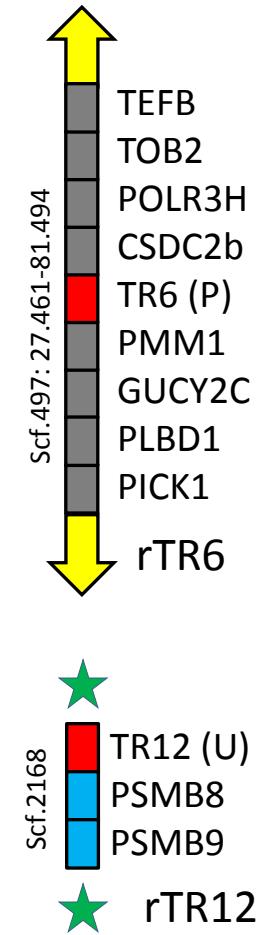
S11



S10

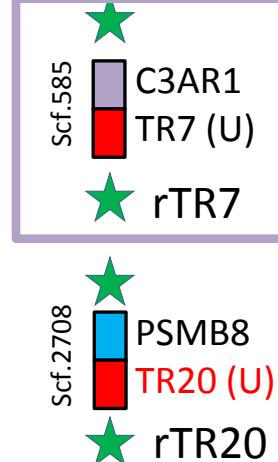


Fugu

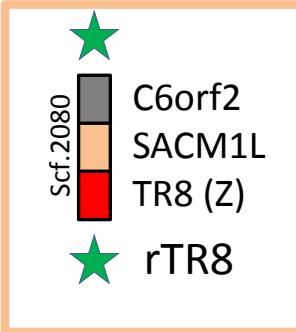


Chromosomal location relates to Fugu5 assembly.

S7



S9



# Spotted gar

